

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/522,753 C  
Source: IFW/6  
Date Processed by STIC: 5/30/06

***ENTERED***



IFW16

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/522,753C

DATE: 06/02/2006  
TIME: 15:51:32

Input Set : A:\SALK1510.APP  
Output Set: N:\CRF4\06022006\I522753C.raw

3 <110> APPLICANT: EVANS, RONALD M.  
4 CHEN, J. DON  
5 ORDENTLICH, PETER  
6 DOWNES, MICHAEL R.  
8 <120> TITLE OF INVENTION: FAMILY OF TRANSCRIPTIONAL CO-REPRESSORS THAT INTERACT  
9 WITH NUCLEAR HORMONE RECEPTORS AND USES THEREFOR  
11 <130> FILE REFERENCE: SALK1510-3  
13 <140> CURRENT APPLICATION NUMBER: 09/522,753C  
14 <141> CURRENT FILING DATE: 2000-03-10  
16 <150> PRIOR APPLICATION NUMBER: 08/522,726  
17 <151> PRIOR FILING DATE: 1995-09-01  
19 <160> NUMBER OF SEQ ID NOS: 52  
21 <170> SOFTWARE: PatentIn Ver. 2.1  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 1495  
25 <212> TYPE: PRT  
26 <213> ORGANISM: Homo sapiens  
28 <400> SEQUENCE: 1  
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30 1 5 10 15  
32 Ala Gln Lys Leu Pro Gly Asp Pro Pro Cys Trp Thr Ser Gly Leu Pro  
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35 Phe Pro Val Pro Pro Arg Glu Val Ile Lys Ala Ser Pro His Ala Pro  
36 35 40 45  
38 Asp Pro Ser Ala Phe Ser Tyr Ala Pro Pro Gly His Pro Leu Pro Leu  
39 50 55 60  
41 Gly Leu His Asp Thr Ala Arg Pro Val Leu Pro Arg Pro Pro Thr Ile  
42 65 70 75 80  
44 Ser Asn Pro Pro Pro Leu Ile Ser Ser Ala Lys His Pro Ser Val Leu  
45 85 90 95  
47 Glu Arg Gln Ile Gly Ala Ile Ser Gln Gly Met Ser Val Gln Leu His  
48 100 105 110  
50 Val Pro Tyr Ser Glu His Ala Lys Ala Pro Val Gly Pro Val Thr Met  
51 115 120 125  
53 Gly Leu Pro Leu Pro Met Asp Pro Lys Lys Leu Ala Pro Phe Ser Gly  
54 130 135 140  
56 Val Lys Gln Glu Gln Leu Ser Pro Arg Gly Gln Ala Gly Pro Pro Glu  
57 145 150 155 160  
59 Ser Leu Gly Val Pro Thr Ala Gln Glu Ala Ser Val Leu Arg Gly Thr  
60 165 170 175  
62 Ala Leu Gly Ser Val Pro Gly Gly Ser Ile Thr Lys Gly Ile Pro Ser  
63 180 185 190  
65 Thr Arg Val Pro Ser Asp Ser Ala Ile Thr Tyr Arg Gly Ser Ile Thr

P.6

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66	195	200	205														
68	His	Gly	Thr	Pro	Ala	Asp	Val	Leu	Tyr	Lys	Gly	Thr	Ile	Thr	Arg	Ile	
69	210		215		220												
71	Ile	Gly	Glu	Asp	Ser	Pro	Ser	Arg	Leu	Asp	Arg	Gly	Arg	Glu	Asp	Ser	
72	225		230		235		240										
74	Leu	Pro	Lys	Gly	His	Val	Ile	Tyr	Glu	Gly	Lys	Lys	Gly	His	Val	Leu	
75			245		250		255										
77	Ser	Tyr	Glu	Gly	Gly	Met	Ser	Val	Thr	Gln	Cys	Ser	Lys	Glu	Asp	Gly	
78		260		265		270											
80	Arg	Ser	Ser	Ser	Gly	Pro	Pro	His	Glu	Thr	Ala	Ala	Pro	Lys	Arg	Thr	
81		275		280		285											
83	Tyr	Asp	Met	Met	Glu	Gly	Arg	Val	Gly	Arg	Ala	Ile	Ser	Ser	Ala	Ser	
84		290		295		300											
86	Ile	Glu	Gly	Leu	Met	Gly	Arg	Ala	Ile	Pro	Pro	Glu	Arg	His	Ser	Pro	
87	305		310		315		320										
89	His	His	Leu	Lys	Glu	Gln	His	His	Ile	Arg	Gly	Ser	Ile	Thr	Gln	Gly	
90		325		330		335											
92	Ile	Pro	Arg	Ser	Tyr	Val	Glu	Ala	Gln	Glu	Asp	Tyr	Leu	Arg	Arg	Glu	
93		340		345		350											
95	Ala	Lys	Leu	Leu	Lys	Arg	Glu	Gly	Thr	Pro	Pro	Pro	Pro	Pro	Pro	Ser	
96		355		360		365											
98	Arg	Asp	Leu	Thr	Glu	Ala	Tyr	Lys	Thr	Gln	Ala	Leu	Gly	Pro	Leu	Lys	
99		370		375		380											
101	Leu	Lys	Pro	Ala	His	Glu	Gly	Leu	Val	Ala	Thr	Val	Lys	Glu	Ala	Gly	
102	385		390		395		400										
104	Arg	Ser	Ile	His	Glu	Ile	Pro	Arg	Glu	Glu	Leu	Arg	His	Thr	Pro	Glu	
105		405		410		415											
107	Leu	Pro	Leu	Ala	Pro	Arg	Pro	Leu	Lys	Glu	Gly	Ser	Ile	Thr	Gln	Gly	
108		420		425		430											
110	Thr	Pro	Leu	Lys	Tyr	Asp	Thr	Gly	Ala	Ser	Thr	Thr	Gly	Ser	Lys	Lys	
111		435		440		445											
113	His	Asp	Val	Arg	Ser	Leu	Ile	Gly	Ser	Pro	Gly	Arg	Thr	Phe	Pro	Pro	
114		450		455		460											
116	Val	His	Pro	Leu	Asp	Val	Met	Ala	Asp	Ala	Arg	Ala	Leu	Glu	Arg	Ala	
117	465		470		475		480										
119	Cys	Tyr	Glu	Glu	Ser	Leu	Lys	Ser	Arg	Pro	Gly	Thr	Ala	Ser	Ser	Ser	
120		485		490		495											
122	Gly	Gly	Ser	Ile	Ala	Arg	Gly	Ala	Pro	Val	Ile	Val	Pro	Glu	Leu	Gly	
123		500		505		510											
125	Lys	Pro	Arg	Gln	Ser	Pro	Leu	Thr	Tyr	Glu	Asp	His	Gly	Ala	Pro	Phe	
126		515		520		525											
128	Ala	Gly	His	Leu	Pro	Arg	Gly	Ser	Pro	Val	Thr	Met	Arg	Glu	Pro	Thr	
129		530		535		540											
131	Pro	Arg	Leu	Gln	Glu	Gly	Ser	Leu	Ser	Ser	Ser	Lys	Ala	Ser	Gln	Asp	
132	545		550		555		560										
134	Arg	Lys	Leu	Thr	Ser	Thr	Pro	Arg	Glu	Ile	Ala	Lys	Ser	Pro	His	Ser	
135		565		570		575											
137	Thr	Val	Pro	Glu	His	His	Pro	His	Pro	Ile	Ser	Pro	Tyr	Glu	His	Leu	
138		580		585		590											

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140 Leu Arg Gly Val Ser Gly Val Asp Leu Tyr Arg Ser His Ile Pro Leu  
141 595 600 605  
143 Ala Phe Asp Pro Thr Ser Ile Pro Arg Gly Ile Pro Leu Asp Ala Ala  
144 610 615 620  
146 Ala Ala Tyr Tyr Leu Pro Arg His Leu Ala Pro Asn Pro Thr Tyr Pro  
147 625 630 635 640  
149 His Leu Tyr Pro Pro Tyr Leu Ile Arg Gly Tyr Pro Asp Thr Ala Ala  
150 645 650 655  
152 Leu Glu Asn Arg Gln Thr Ile Ile Asn Asp Tyr Ile Thr Ser Gln Gln  
153 660 665 670  
155 Met His His Asn Thr Ala Thr Ala Met Ala Gln Arg Ala Asp Met Leu  
156 675 680 685  
158 Arg Gly Leu Ser Pro Arg Glu Ser Ser Leu Ala Leu Asn Tyr Ala Ala  
159 690 695 700  
161 Gly Pro Arg Gly Ile Ile Asp Leu Ser Gln Val Pro His Leu Pro Val  
162 705 710 715 720  
164 Leu Val Pro Pro Thr Pro Gly Thr Pro Ala Thr Ala Met Asp Arg Leu  
165 725 730 735  
167 Ala Tyr Leu Pro Thr Ala Pro Gln Pro Phe Ser Ser Arg His Ser Ser  
168 740 745 750  
170 Ser Pro Leu Ser Pro Gly Gly Pro Thr His Leu Thr Lys Pro Thr Thr  
171 755 760 765  
173 Thr Ser Ser Ser Glu Arg Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg  
174 770 775 780  
176 Asp Arg Glu Arg Glu Lys Ser Ile Leu Thr Ser Thr Thr Thr Val Glu  
177 785 790 795 800  
179 His Ala Pro Ile Trp Arg Pro Gly Thr Glu Gln Ser Ser Gly Ser Ser  
180 805 810 815  
182 Gly Ser Ser Gly Gly Gly Gly Ser Ser Ser Arg Pro Ala Ser His  
183 820 825 830  
185 Ser His Ala His Gln His Ser Pro Ile Ser Pro Arg Thr Gln Asp Ala  
186 835 840 845  
188 Leu Gln Gln Arg Pro Ser Val Leu His Asn Thr Gly Met Lys Gly Ile  
189 850 855 860  
191 Ile Thr Ala Val Glu Pro Ser Lys Pro Thr Val Leu Arg Ser Thr Ser  
192 865 870 875 880  
194 Thr Ser Ser Pro Val Arg Pro Ala Ala Thr Phe Pro Pro Ala Thr His  
195 885 890 895  
197 Cys Pro Leu Gly Gly Thr Leu Asp Gly Val Tyr Pro Thr Leu Met Glu  
198 900 905 910  
200 Pro Val Leu Leu Pro Lys Glu Ala Pro Arg Val Ala Arg Pro Glu Arg  
201 915 920 925  
203 Pro Arg Ala Asp Thr Gly His Ala Phe Leu Ala Lys Pro Pro Ala Arg  
204 930 935 940  
206 Ser Gly Leu Glu Pro Ala Ser Ser Pro Ser Lys Gly Ser Glu Pro Arg  
207 945 950 955 960  
209 Pro Leu Val Pro Pro Val Ser Gly His Ala Thr Ile Ala Arg Thr Pro  
210 965 970 975  
212 Ala Lys Asn Leu Ala Pro His His Ala Ser Pro Asp Pro Pro Ala Pro

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213 980 985 990  
 215 Pro Ala Ser Ala Ser Asp Pro His Arg Glu Lys Thr Gln Ser Lys Pro  
 216 995 1000 1005  
 218 Phe Ser Ile Gln Glu Leu Glu Leu Arg Ser Leu Gly Tyr His Gly Ser  
 219 1010 1015 1020  
 221 Ser Tyr Ser Pro Glu Gly Val Glu Pro Val Ser Pro Val Ser Ser Pro  
 222 1025 1030 1035 1040  
 224 Ser Leu Thr His Asp Lys Gly Leu Pro Lys His Leu Glu Glu Leu Asp  
 225 1045 1050 1055  
 227 Lys Ser His Leu Glu Gly Glu Leu Arg Pro Lys Gln Pro Gly Pro Val  
 228 1060 1065 1070  
 230 Lys Leu Gly Gly Glu Ala Ala His Leu Pro His Leu Arg Pro Leu Pro  
 231 1075 1080 1085  
 233 Glu Ser Gln Pro Ser Ser Pro Leu Leu Gln Thr Ala Pro Gly Val  
 234 1090 1095 1100  
 236 Lys Gly His Gln Arg Val Val Thr Leu Ala Gln His Ile Ser Glu Val  
 237 1105 1110 1115 1120  
 239 Ile Thr Gln Asp Tyr Thr Arg His His Pro Gln Gln Leu Ser Ala Pro  
 240 1125 1130 1135  
 242 Leu Pro Ala Pro Leu Tyr Ser Phe Pro Gly Ala Ser Cys Pro Val Leu  
 243 1140 1145 1150  
 245 Asp Leu Arg Arg Pro Pro Ser Asp Leu Tyr Leu Pro Pro Pro Asp His  
 246 1155 1160 1165  
 248 Gly Ala Pro Ala Arg Gly Ser Pro His Ser Glu Gly Gly Lys Arg Ser  
 249 1170 1175 1180  
 251 Pro Glu Pro Asn Lys Thr Ser Val Leu Gly Gly Glu Asp Gly Ile  
 252 1185 1190 1195 1200  
 254 Glu Pro Val Ser Pro Pro Glu Gly Met Thr Glu Pro Gly His Ser Arg  
 255 1205 1210 1215  
 257 Ser Ala Val Tyr Pro Leu Leu Tyr Arg Asp Gly Glu Gln Thr Glu Pro  
 258 1220 1225 1230  
 260 Ser Arg Met Gly Ser Lys Ser Pro Gly Asn Thr Ser Gln Pro Pro Ala  
 261 1235 1240 1245  
 263 Phe Phe Ser Lys Leu Thr Glu Ser Asn Ser Ala Met Val Lys Ser Lys  
 264 1250 1255 1260  
 266 Lys Gln Glu Ile Asn Lys Lys Leu Asn Thr His Asn Arg Asn Glu Pro  
 267 1265 1270 1275 1280  
 269 Glu Tyr Asn Ile Ser Gln Pro Gly Thr Glu Ile Phe Asn Met Pro Ala  
 270 1285 1290 1295  
 272 Ile Thr Gly Thr Gly Leu Met Thr Tyr Arg Ser Gln Ala Val Gln Glu  
 273 1300 1305 1310  
 275 His Ala Ser Thr Asn Met Gly Leu Glu Ala Ile Ile Arg Lys Ala Leu  
 276 1315 1320 1325  
 278 Met Gly Lys Tyr Asp Gln Trp Glu Glu Ser Pro Pro Leu Ser Ala Asn  
 279 1330 1335 1340  
 281 Ala Phe Asn Pro Leu Asn Ala Ser Ala Ser Leu Pro Ala Ala Met Pro  
 282 1345 1350 1355 1360  
 284 Ile Thr Ala Ala Asp Gly Arg Ser Asp His Thr Leu Thr Ser Pro Gly  
 285 1365 1370 1375

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287 Gly Gly Gly Lys Ala Lys Val Ser Gly Arg Pro Ser Ser Arg Lys Ala  
288 1380 1385 1390  
290 Lys Ser Pro Ala Pro Gly Leu Ala Ser Gly Asp Arg Pro Pro Ser Val  
291 1395 1400 1405  
293 Ser Ser Val His Ser Glu Gly Asp Cys Asn Arg Arg Thr Pro Leu Thr  
294 1410 1415 1420  
296 Asn Arg Val Trp Glu Asp Arg Pro Ser Ser Ala Gly Ser Thr Pro Phe  
297 1425 1430 1435 1440  
299 Pro Tyr Asn Pro Leu Ile Met Arg Leu Gln Ala Gly Val Met Ala Ser  
300 1445 1450 1455  
302 Pro Pro Pro Gly Leu Pro Ala Gly Ser Gly Pro Leu Ala Gly Pro  
303 1460 1465 1470  
305 His His Ala Trp Asp Glu Glu Pro Lys Pro Leu Leu Cys Ser Gln Tyr  
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309 1490 1495  
312 <210> SEQ ID NO: 2  
313 <211> LENGTH: 46  
314 <212> TYPE: PRT  
315 <213> ORGANISM: Homo sapiens  
317 <400> SEQUENCE: 2  
318 His Ser Asp Val Ser Glu Ser Lys Arg Lys Arg Phe Glu Leu Asn Ser  
319 1 5 10 15  
321 Gly Glu Ala Gly Gly Asn Ala Thr Ser Ala Met Thr Asn Ser Ser Thr  
322 20 25 30  
324 Ser Gly Ser Met Asn Ile Ser Asn Ser His Gly Leu Lys Ala  
325 35 40 45  
328 <210> SEQ ID NO: 3  
329 <211> LENGTH: 17  
330 <212> TYPE: DNA  
331 <213> ORGANISM: Saccharomyces sp.  
333 <400> SEQUENCE: 3  
334 cggaggactg tcctccg 17  
337 <210> SEQ ID NO: 4  
338 <211> LENGTH: 8561  
339 <212> TYPE: DNA  
340 <213> ORGANISM: Homo sapiens  
342 <400> SEQUENCE: 4  
343 catgtcgggc tccacacagc ttgtggcaca gacgtggagg gccactgagc cccgctaccc 60  
344 gccccacagc ctttcctacc cagtgcagat cgccggacg cacacggacg tcgggctcct 120  
345 ggagtaccag caccactccc gcgactatgc ctcccacctg tcgcccggct ccatcatcca 180  
346 gccccagcgg cggaggccct ccctgtgtc tgagttccag cccggaaatg aacggtccca 240  
347 ggagctccac ctgcggccag agtcccactc atacctgccc gagctggga agtcagagat 300  
348 ggagttcatt gaaagcaagc gcccctcgct agagctgtc cctgacccccc tgctgcgacc 360  
349 gtcacccctg ctggccacgg gccagcctgc gggatctgaa gacctcacca aggaccgtag 420  
350 cctgacgggc aagcttggAAC cggtgtctcc ccccaGGGGCC cccgacactg accctgagct 480  
351 ggagctgggt cccgcacggc tgtccaagga ggagctgtac cagaacatgg accgcgtgga 540  
352 ccgagagatc accatggtag agcagcagat ctctaagctg aagaagaagc agcaacagct 600  
353 ggaggaggag gctgccaagc cggccgagcc tgagaagccc gtgtcaccgc cggccatcga 660

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/02/2006  
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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; N Pos. 109,8173,8180,8302,8343,8359,8384

Seq#:8; N Pos. 7250,7257,7379,7420,7436,7461

**VERIFICATION SUMMARY**

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L:1011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:60

M:341 Repeated in SeqNo=6

L:1780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:7200

M:341 Repeated in SeqNo=8